

OW of: US-09-652-292-2 to: EST:* out_format : pfs

Date: Mar 15, 2002 7:30 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL-frame p2n.model -DEV-xmlh
-Q/cgna2/USPTO.spool/US09652292/runat_13032002_161725_3195/app_query.fasta_1.606
-DB-EST -QFMT-fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -CGAPOP=4.500
-CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FCGPOP=6.000
-FCGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09652292_CGNN1_1.4076
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-652-292-2
Query length: 541
Database: EST.*
Database sequences: 11351937
Database length: 1077921985
Search time (sec): 1204.940000

score_list:

Sequence	Strd	Orig	zScore	EScore	Len	Documentation ...
gb_est1.AL554162	+	1163.50	1484.02	1.7e-73	910	AL554162 AL554162 LTI_NFL006_PL2
gb_est1.AL449917	-	786.00	1007.12	6.2e-47	466	AL449914 AL449914 Homo sapiens
gb_est1.AL449887	-	781.00	1000.87	1.4e-46	459	AL449887 AL449887 Homo sapiens
gb_est1.AL449913	+	770.00	986.75	8.5e-46	461	AL449913 AL449913 Homo sapiens
gb_est1.AL449886	+	742.00	931.14	8.2e-44	450	AL449886 AL449886 Homo sapiens
gb_est1.BE327601	+	689.00	881.62	6.1e-40	540	BE327601 146953 MARC 4BOV Bos t
gb_est2.BF688799	+	623.00	791.00	6.8e-35	1049	BF688799 602184982F1 NIH_MGC_4
gb_est2.BF706976	+	553.00	708.65	2.6e-30	481	BF706976 281657 MARC 3BOV Bos t
gb_est1.AA313045	+	473.00	610.46	7.7e-25	306	AA313045 EST183920 Pancreas tum
gb_est1.AL449905	-	445.00	572.10	1.1e-22	402	AL449905 AL449905 Homo sapiens
gb_est2.BF615211	+	433.50	555.12	9.3e-22	513	BF615211 G082804.x1 Wellcome CR
gb_est2.BF612918	+	403.00	516.50	1.3e-19	491	BF612918 G078801.x2 Wellcome CR
gb_hcc.AK005068	+	403.00	501.27	9.3e-19	2538	AK005068 Mus musculus adult ma
gb_est1.AL449904	+	398.00	512.09	2.3e-19	396	AL449904 AL449904 Homo sapiens
gb_est1.AG14852	+	377.00	489.56	4.2e-18	248	AG14852 vF95G08.y1 Soares mam
gb_est2.BF611497	-	358.00	455.74	3.2e-16	691	BF611497 G082804.y1 Wellcome CR
gb_gss.CNS049BV	+	353.00	446.24	1.1e-15	966	AL280372 Tetraodon nigroviridis
gb_est2.BF789282	+	332.00	421.74	2.5e-14	747	BF789282 G02105191F1 NCI_CGAP_X
gb_est1.AA415084	+	332.00	412.60	8.1e-14	2003	AA415084 M90018 RCW Lambda Zap
gb_est1.AL118747	+	320.50	408.73	1.3e-13	622	AL118747 DRF2P76100210.rl 761
gb_est2.BF611325	-	315.50	401.15	3.5e-13	706	BF611325 G078801.y1 Wellcome CR
gb_est1.AV384186	+	311.00	395.41	7.3e-13	705	AV384186 AV384186 Halocynthia r
gb_est1.AW586065	+	303.50	386.27	2.4e-12	671	AW586065 EST317688 MHAM Medicag
gb_est1.BE641687	-	298.00	377.25	7.5e-12	831	BE641687 Cr12_3_P16_SP6 Ceratop
gb_est1.AL449468	-	294.00	384.66	2.9e-12	215	AL449468 AL449468 Homo sapiens
gb_est1.AL449471	-	293.00	382.64	3.8e-12	233	AL449471 AL449471 Homo sapiens
gb_est1.AL449916	-	291.00	381.00	4.7e-12	211	AL449916 AL449916 Homo sapiens
gb_est1.BE642082	+	291.00	368.93	2.2e-11	775	BE642082 Cr12_5_B13_SP6 Ceratop
gb_est1.AA461907	+	289.00	378.75	6.2e-12	204	AA461907 vF95G08.y1 Soares mam
gb_est2.BF328407	+	288.50	377.98	6.9e-12	207	BF328407 PM3-BN0174-230500-006
gb_est1.AW657233	+	285.00	364.45	3.9e-11	549	AW657233 109952 MARC 1BOV Bos t
gb_est1.AL449891	+	284.00	373.51	1.2e-11	180	AL449891 AL449891 Homo sapiens
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gb_est1.AV383222	+	280.50	355.85	1.2e-10	746	AV383222 AV383222 Halocynthia r
gb_est2.BF033803	+	279.50	353.65	1.6e-10	824	BF033803 G01454148F1 NIH_MGC_6
gb_est1.AW934681	+	275.50	349.88	2.5e-10	712	AW934681 EST353573 tomato flowe
gb_est1.AW940827	-	275.00	347.55	3.4e-10	855	AW940827 GH21490.3prime GH Dro
gb_gss.AQ989426	+	274.50	341.03	2.2e-10	548	AQ989426 Gm_UMB001.157_J16F UMN
gb_gss.CNS06VUO	-	273.00	343.53	5.7e-10	1000	AL417624 T7 end of clones AX0A
gb_est2.R59842	+	272.00	348.27	3.1e-10	523	R59842 yhl1908.rl Soares infan

gb_gss.CNS06WME - 270.50 339.85 9.1e-10 1054 ! AL405660 T3 end of clone AU
gb_est1.AL449917 - 267.00 349.98 2.5e-10 218 ! AL449917 AL449917 Homo sapie
gb_est1.AL449467 - 264.00 347.61 3.4e-10 186 ! AL449467 AL449467 Homo sapie
gb_est2.BI268049 + 264.00 335.84 1.5e-09 662 ! BI268049 NF119G09IN1F1072 In
gb_est2.BE910478 + 262.50 330.73 2.9e-09 934 ! BE910478 601501005F1 NIH_MGC
seq_name: gb_est1.AL554162
seq_documentation_block:
LOCUS AL554162 910 bp mRNA EST 16-FEB-2001
DEFINITION AL554162 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI081YA24 5
prime, mRNA sequence.
ACCESSION AL554162
VERSION AL554162.1 GI:12894675
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 910)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. 910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI081YA24"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site: 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com.
BASE COUNT 115 a 282 c 264 g 222 t 27 others
ORIGIN
alignment_scores:
Quality: 1163.50 Length: 281
Ratio: 4.458 Gaps: 4
Percent Similarity: 92.883 Percent Identity: 90.391
alignment_block:
US-09-652-292-2 x AL554162 ..
Align seg 1/1 to: AL554162 from: 1 to: 910
1 MetGlyHisSerProProValLeuProLeuCysAlaSerValSerLeuLe 17
72 ATGGGGCACTTCACCTGTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 121
17 uGly...GlyLeuThrPhedGlyTyrGluLeuAlaValIleSerGlyAlaL 33
122 GGGCTGTGGCTGACCTTTGGTTATCACTGGYMGVYATATCAGGTGCC 171
33 euLeuProLeuGluLeuAapphe.....GlyLeuSerCysLeuGluGln 47
172 TGTGTGCACCTGCAGCTTGACTTTTGGGCTAWKCTKYTTTTTWTYTKAT 221
48 GluPheLeuValGlySerLeuLeuGlyAlaLeuLeuAlaSerLeuVa 64
222 TCCTKTKTKKGCAGCTGCTCCTTGGGGGYTCCTCTCTCCTCCCTGGT 271


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VERSION AL449887.1 GI:11181512
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 459)
JOURNAL Stavrvides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished. Stavrvides,G.S., Huckle,E.J. and Deloukas,P
Contact: Stavrvides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccd1338.
FEATURES
source
1..459
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrvides GS)"
/tissue_type="Lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 74 a 148 c 142 g 95 t
ORIGIN

alignment_scores:
Quality: 781.00 Length: 153
Ratio: 5.105 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.346

alignment_block:
US-09-652-292-2 x AL449887
Align seg 1/1 to: AL449887 from: 1 to: 459
162 TrpGlyTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeuGI 178
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1 TGGGGATGAGGCACATGTTGGCTGGGCCACTGCACCTGCTCTCTGCA 50
|||||
178 nSerLeuSerLeuLeuPheLeuProAlaGlyThrAspGluThrAlaThrH 195
|||||
51 ATCCCTCAGCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 100
|||||
195 isLysAspLeuIleProLeuGlnGlyGlyAlaProLysLeuGlyPro 211
|||||
101 ACAAGGACCTCATCCACATCCAGGGAGGTGAGGCCGCCCAAGCTGGCCCG 150
|||||
212 GlyArgProArgTy;SerPheLeuAspLeuPheArgAlaAspAsnMe 228
|||||
151 GGGAGCCACGGTACTCTCTTTCTGGACCTCTTCAGGCGCAGCGATAACAT 200
|||||
228 tArgGlyArgThrThrValGlyLeuGlyLeuValLeuPheGlnGlnLeuT 245
|||||
201 GCGAGCCGCGACACAGTGGGCTGGGCTGGTCTCTTCCAGCAACTAA 250
|||||
245 hrGlyGlnProAsnValLeuCysTyThrAlaSerThrIlePheSerVal 261
|||||
251 CAGGGCGGCCCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
|||||
262 GlyPheHisGlyGlySerSerAlaValLeuAlaSerValGlyGlyAl 278
|||||
301 GGTTCATGGGGATCCTCAGCCGCTGCTGGCTCTGTGGGCTGGCCG 350
|||||
278 aValLysValAlaAlaThrLeuThrAlaMetGlyLeuValAspArgAlaG 295
|||||
351 AGTGAAGTGGCAGCTACCTGACCCCATGGGCTGGTGGGCGGCGAG 400
|||||
295 lyArgArgAlaLeuLeuAlaGlyCysAlaLeuMetAlaLeuSerVal 311
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401 GCCGCAAGCCTCTGTGCTAGCTGGCTGTGCCCTCATGGCCCTGTCCGTC 450
312 SerGlyIle 314
|||||
451 ACTGGCATA 459
seq_name: gb_est1:AL449913
seq_documentation_block: 461 bp mRNA EST 15-NOV-2000
LOCUS AL449913 Homo sapiens fetal lung (Stavrvides GS) Homo sapiens cDNA,
DEFINITION AL449913 Homo sapiens fetal lung (Stavrvides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449913
VERSION AL449913.1 GI:11181538
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 461)
JOURNAL Stavrvides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished. Stavrvides,G.S., Huckle,E.J. and Deloukas,P
Contact: Stavrvides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccd3334.
FEATURES
source
1..461
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrvides GS)"
/tissue_type="Lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 56 a 146 c 145 g 114 t
ORIGIN

alignment_scores:
Quality: 770.00 Length: 153
Ratio: 5.033 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-652-292-2 x AL449913
Align seg 1/1 to: AL449913 from: 1 to: 461
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|||||
2 TCAGGTGCCCTGCTGCCACTGCAGCTTGACTTTGGGCTAAGCTGCTTGA 51
|||||
46 uGlnGluPheLeuValGlySerLeuLeuGlyAlaLeuLeuAlaSerL 63
|||||
52 GCAGGAGTTCTTGGTGGCAGCCTGCTCTCTGGGGCTCTCTCGCCCTCC 101
|||||
63 euValGlyGlyPheLeuIleAspCysTyThrGlyArgLysGlnAlaIleLeu 79
|||||
102 TGGTTGGCTTCTCTCATTTGACTGTGATGGCAGGACGCTGACCTGGCTG 151
|||||
80 GlySerAsnLeuValLeuLeuAlaGlySerLeuThrLeuGlyLeuAlaGI 96
|||||
152 GGGAGCAACTTGGTGTCTGCTGGCAGCAGCCTGACCTGGCTGGCTGGT 201
|||||
96 ySerLeuAlaThrLeuValLeuGlyArgAlaValValGlyPheAlaIle 113
|||||
202 TTCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTTT 251
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113 erLeuSerSerMetAlaCysCysIleTyrValSerGluLeuValGlyPro 129
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```

9

3

Library made from pooled tissue from day 20 and day 40 embryos."

BASE COUNT 57 a 189 c 176 g 118 t

alignment_scores:
Quality: 689.00 Length: 165
Ratio: 4.389 Gaps: 0
Percent Similarity: 95.152 Percent Identity: 87.273

alignment_block:
US-09-652-292-2 x BE237601

Align seg 1/1 to: BE237601 from: 1 to: 540

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1 MetGlyHisSerProProValLeuProLeuCysAlaSerValSerLeuLe 17
|||||:  :::::|||||
47 ATGGCGGACCTTCACTCTCTGCGCTCTGTGCGCTCGTGTCTTGTCT 96
|||||:  :::::|||||
17 uGlyGlyLeuThrPheGlyTyrGluLeuAlaValIleSerGlyAlaLeu 34
|||||:  :::::|||||
97 GGGTGGCCTGACCTTGGGTATGAACATGGCAGTCATATCGGTGCGCTGC 146
|||||:  :::::|||||
34 euProLeuGlnLeuAspPheGlyLeuSerCysLeuGluGlnGluPheLeu 50
|||||:  :::::|||||
147 TGGCGCTGACGCTGATTTGGCGCTGAGCTGCTCAGCAGGAGGCTTCG 196
|||||:  :::::|||||
51 ValGlySerLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPh 67
|||||:  :::::|||||
197 GTGGCGACCTGCTCTCGGGGCTCTCTTGCCTCGCTAGGGGGCTG 246
|||||:  :::::|||||
67 eLeuIleAspCysTyrGlyArgLysGlnAlaIleLeuGlySerAsnLeu 84
|||||:  :::::|||||
247 CCTCATCGACCGCTATGGCGGAAGCAAGCCATCTCGGAGCAACTTGG 296
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84 alLeuLeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrp 100
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297 TGTGTGGCAGCAGCCTGAGCTGGGCTGGCGGCTGCGGCTGCTGCTG 346
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101 LeuValLeuGlyArgAlaValValGlyPheAlaIleSerLeuSerSerMe 117
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347 CTGCTCTGGCGGCTCGGTGGCTGCTTTTGCCATCTCCCTCTCCCTCAT 396
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117 tAlaCysCysIleTyrValSerGluLeuValGlyProArgGlnArgGly 134
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397 GGCTCTGCTGATCAGCTGTCTCAGCTGGCGGCGCCACGCGCGGGAG 446
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134 alLeuValSerLeuTyrGluAlaGlyIleThrValGlyIleLeuSer 150
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447 TGTGTGGCAGCAGCCTGAGCTGGGCTGGCGGCTGCGGCTGCTGCTC 495
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151 TyrAlaLeuAsnTyrAlaLeuAlaGlyThrProTyrGlyTyrArg 165
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496 TAGCGCCTCAACTATGCACTGGCGGCGGCGCCCGCGGATGGAGG 540
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seq_name: gb_est2:BF688799

seq_documentation_block: 1049 bp mRNA EST 22-DEC-2000
LOCUS BF688799 602184982P1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299237 5',
DEFINITION mRNA sequence.

ACCESSION BF688799
VERSION BF688799.1 GI:11974207
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1049)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1156 row: d column: 22

High quality sequence stop: 635.

FEATURES
Location/Qualifiers
source

1..1049

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4299237"

/clone_lib="NIH_MGC_43"

/tissue_type="normal pigmented retinal epithelium"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOH7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. I"

BASE COUNT 231 a 331 c 229 g 258 t

ORIGIN

alignment_scores:

Quality: 623.00 Length: 122

Ratio: 5.107 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.180

alignment_block:

US-09-652-292-2 x BF688799

Align seg 1/1 to: BF688799 from: 1 to: 1049

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420 ValSerAlaPheSerPheGlyPheGlyProValThrTrpLeuValLeuSe 436
|||||:  :::::|||||
5 GTCACTGCGCTTCTCTTGGTTAGGGCCAGTACCTGGCTTGTCTCTCAG 54
|||||:  :::::|||||
436 rGluIleTyrProValGluIleArgGlyArgAlaPheAlaPheCysAsnS 453
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55 CGAGATCTACCCCTGTGGAGATACGAGGAGAGAGCGCTTCGCTTCTGCAACA 104
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453 erPheAsnTrpAlaAlaAsnLeuPheIleSerLeuSerPheLeuAspLeu 459
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105 GCYTCAACTGGCGGCGCAACCTCTTCATCAGCCTCTCTCTCTCGATCTC 154
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470 IleGlyThrIleGlyLeuSerTrpThrPheLeuLeuTyrGlyLeuThrAl 486
|||||:  :::::|||||
155 ATTGGCACCATCGGCTGTCTCGGACCTTCTCTCTACGGAGCTGACCGC 204
|||||:  :::::|||||
486 aValLeuGlyLeuGlyPheIleTyrLeuPheValProGluThrLysGlyG 503
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205 TGTCTCTGGCGCTGGGCTTCTATCTATTTATTTGTTCTGAAACAAAGGCC 254
|||||:  :::::|||||
503 InSerLeuAlaGluIleAspGlnPheGlnLysArgArgPheThrLeu 519
|||||:  :::::|||||
255 AGTCGTGGCAGAGATAGACCAGCAGTTCAGAGAGAGAGCGGTTCACCCCTG 304
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520 SerPheGlyHisArgGlnAsnSerThrGlyIleProTyrSerArgIleGl 536
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305 AGCTTGGGCACAGGAGCAACTCCACTGGCATCCCGTACAGCGCATCGA 354
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536 uIleSerAlaAlaSer 541
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355 GATCTCTGGCGCTCC 370
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/dev_stage="adult"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
BASE COUNT 61 a 95 c 72 g 73 t 5 others
ORIGIN

alignment_scores:
Quality: 473.00 Length: 96
Ratio: 5.032 Gaps: 0
Percent Similarity: 97.917 Percent Identity: 95.833

alignment_block:
US-09-652-292-2 x AA313045 ..

Align seg 1/1 to: AA313045 from: 1 to: 306

444 ATGGTGAAGAGGAGGCTTCGCTTCGACACAGCTTCACTGGCGGCCAACCT 460
1 CGAGGAGAGGCTTCGCTTCGACACAGCTTCACTGGCGGCCAACCT 50
460 uPheLeuSerLeuSerPheLeuAspLeuLeuGlyThrLeuGlyLeuSerT 477
51 CTTTCATCAGCCTCTCTCTCTCGATCTCATTTGGCACCATCGGCTTGTCT 100
477 rPThrPheLeuLeuTyrGlyLeuThrAlaValLeuGlyLeuGlyPheLeu 493
101 GGACCTTCTCTCTACGAGCTGACGCTGCTCTCGGCTGGGCTTCATC 150
494 TyrLeuPheValProGluThrGlyGlnSerLeuAlaGluLeuAspGly 510
151 TATTTATTTTGTCTTCAACAAAGCCAGTCTGTCGACAGATAGACCA 200
510 nGlnPheGlnLysArgPheThrLeuSerPheGlyHisArgGlnAsnS 527
201 GCAGTTNCAGAGAGAGCGTTTCACTGAGCTTNGCCAGGACGAGAACT 250
527 eThrGlyLeuProTyrSerArgIleGluLeuSerAla 539
251 CCACCTGGCATCCGTACAGCGCATCGAGATCTCTGCG 288

seq_name: gb_est1:AL449905

seq_documentation_block:
LOCUS AL449905 402 bp mRNA EST 15-NOV-2000
DEFINITION AL449905 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449905
VERSION AL449905.1 GI:11181530
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 402)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name: scc3095.
Location/Qualifiers
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/map="20"
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/tissue_type="Lung"
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/note="cDNA fragment isolated using a cDNA end rescue technique"

FEATURES
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469 uLLeGlyThrIleGlyLeuSerTrpThrPheLeuLeuTyrGlyLeuThrA 486
347 CATTTGGCACCATCGGCTTGTCTGGACCTTCTCTACGGACTGACCG 298
486 laValLeuGlyLeuGlyPheLeuTyrLeuPheValProGluThrLysGly 502
297 CTGCTCTCGGCTGGGCTTCATCTATTATTGTTCTTCAACAAAGGC 248
503 GlnSerLeuAlaGluLeuAspGlnGlnPheGlnLysArgPheThrLe 519
247 CAGTCCTTGGCAGAGATAGACAGCAGTTCACAGAGAGCGGTTACACCT 198
519 uSerPheGlyHisArgGlnAsnSerThrGlyIleProTyrSerArgIleG 536
197 GAGCTTGGCCACAGCAGAACTCCACTGGCATCCGCTACAGCCGATCG 148
536 luIleSerAlaAlaSer 541
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sequence.
ACCESSION BF615211
VERSION BF615211.1 GI:11788593
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 513)
AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Willson,R.
TITLE WashU Xenopus EST project, 1999
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: dd82a04.y1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gordon, (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

[illegible]

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1272	TT.....	1273
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1274GTGCTGGTGATAA.....	1288
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mRNA sequence.		
ACCESSION	AL449904	

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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 396)
JOURNAL Stavrides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
Unpublished (2000)
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccd3094.
FEATURES
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52 CCTGCTCTACGGACTACCGCTGCTCGCGCTTCATCTATTAT 101
496 heValProGluThrLysGlyGlnSerLeuAlaGluIleAspGlnPhe 512
102 TTGTTCTTCAACAAAGGCCAGCTGTTGGCAGAGATAGACCAAGCTTC 151
513 GlnLysArgArgPheThrLeuSerPheGlyHisArgGlnAsnSerThrGI 529
152 CAGAAGACAGCGTTACCTGAGCTTTGGCCACAGCAGACACTCCACTGG 201
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ACCESSION AI614852
VERSION AI614852.1 GI:4624019
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SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 248)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:503734
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
Seq primer: -40RP from Glibco
High quality sequence stop: 243.
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        primer [5'
        TGTACCAATCTGAAGTGGAGCGCGCGAATGGTTTGTTCCTTTTTCCTTTTTCCTTTT
        T 3']; double-stranded cDNA was ligated to Eco RI
        adaptors (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of the modified pT73 vector.
        RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
        constructed and normalized by Bento Soares and M.Patina
        Bonaldo."
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52 CTTTATCAGCCTCTCTCTCGACCTGATCGGTGCGCTTGGCTTGGCTT 101
477 rpThrPheLeuLeuTyrrGlyLeuThrAlaValLeuGlyLeuGlyPheIle 493
102 GGACCTTCCTGCTCTATGGCTGACCGCTGCTCTGGCTTGGCTTTCATC 151
494 TyrLeuPheValProGluThrLysGlyGlnSerLeuAlaGluIleAspGI 510
152 TACCTACTTGTCTCTCAACCAAGGACAGCTCTTTAGCTGAATAGACGA 201
510 nGlnPheGlnLysArgArgPheThrLeuSerPheGlyHisArgGln 525
202 GCAGTTTCAGACAAGCAGGTTCCCTCTAAACTTTGGCCATAGGCAG 247

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